

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 10/533,124

Source: PCT/10

Date Processed by STIC: 5/10/05

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PCT

RAW SEQUENCE LISTING

DATE: 05/10/2005

PATENT APPLICATION: US/10/533,124

TIME: 13:30:56

Input Set : A:\SEQ LISTING-2 (WSU-9 US).txt

Output Set: N:\CRF4\05102005\J533124.raw

3 <110> APPLICANT: TERLECKY, Stanley R.
 4 WALTON, Paul A.
 6 <120> TITLE OF INVENTION: PROMOTION OF PEROXISOMAL CATALASE FUNCTION IN CELLS
 8 <130> FILE REFERENCE: 28928.0009)
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/533,124
 12 <141> CURRENT FILING DATE: 2005-04-29
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/34512
 15 <151> PRIOR FILING DATE: 2003-10-30
 17 <150> PRIOR APPLICATION NUMBER: US 60/422,100
 18 <151> PRIOR FILING DATE: 2002-10-30
 20 <160> NUMBER OF SEQ ID NOS: 21
 22 <170> SOFTWARE: PatentIn Ver. 3.2
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 4
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 31 peptide
 33 <400> SEQUENCE: 1
 34 Lys Ala Asn Leu
 35 1
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 527
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Homo sapiens
 43 <400> SEQUENCE: 2
 44 Met Ala Asp Ser Arg Asp Pro Ala Ser Asp Gln Met Gln His Trp Lys
 45 1 5 10 15
 47 Glu Gln Arg Ala Ala Gln Lys Ala Asp Val Leu Thr Thr Gly Ala Gly
 48 20 25 30
 50 Asn Pro Val Gly Asp Lys Leu Asn Val Ile Thr Val Gly Pro Arg Gly
 51 35 40 45
 53 Pro Leu Leu Val Gln Asp Val Val Phe Thr Asp Glu Met Ala His Phe
 54 50 55 60
 56 Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ala Gly
 57 65 70 75 80
 59 Ala Phe Gly Tyr Phe Glu Val Thr His Asp Ile Thr Lys Tyr Ser Lys
 60 85 90 95
 62 Ala Lys Val Phe Glu His Ile Gly Lys Lys Thr Pro Ile Ala Val Arg
 63 100 105 110
 65 Phe Ser Thr Val Ala Gly Glu Ser Gly Ser Ala Asp Thr Val Arg Asp
 66 115 120 125

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68 Pro Arg Gly Phe Ala Val Lys Phe Tyr Thr Glu Asp Gly Asn Trp Asp
69      130                      135                      140
71 Leu Val Gly Asn Asn Thr Pro Ile Phe Phe Ile Arg Asp Pro Ile Leu
72 145                      150                      155                      160
74 Phe Pro Ser Phe Ile His Ser Gln Lys Arg Asn Pro Gln Thr His Leu
75                      165                      170                      175
77 Lys Asp Pro Asp Met Val Trp Asp Phe Trp Ser Leu Arg Pro Glu Ser
78                      180                      185                      190
80 Leu His Gln Val Ser Phe Leu Phe Ser Asp Arg Gly Ile Pro Asp Gly
81                      195                      200                      205
83 His Arg His Met Asn Gly Tyr Gly Ser His Thr Phe Lys Leu Val Asn
84      210                      215                      220
86 Ala Asn Gly Glu Ala Val Tyr Cys Lys Phe His Tyr Lys Thr Asp Gln
87 225                      230                      235                      240
89 Gly Ile Lys Asn Leu Ser Val Glu Asp Ala Ala Arg Leu Ser Gln Glu
90                      245                      250                      255
92 Asp Pro Asp Tyr Gly Ile Arg Asp Leu Phe Asn Ala Ile Ala Thr Gly
93                      260                      265                      270
95 Lys Tyr Pro Ser Trp Thr Phe Tyr Ile Gln Val Met Thr Phe Asn Gln
96                      275                      280                      285
98 Ala Glu Thr Phe Pro Phe Asn Pro Phe Asp Leu Thr Lys Val Trp Pro
99      290                      295                      300
101 His Lys Asp Tyr Pro Leu Ile Pro Val Gly Lys Leu Val Leu Asn Arg
102 305                      310                      315                      320
104 Asn Pro Val Asn Tyr Phe Ala Glu Val Glu Gln Ile Ala Phe Asp Pro
105                      325                      330                      335
107 Ser Asn Met Pro Pro Gly Ile Glu Ala Ser Pro Asp Lys Met Leu Gln
108                      340                      345                      350
110 Gly Arg Leu Phe Ala Tyr Pro Asp Thr His Arg His Arg Leu Gly Pro
111                      355                      360                      365
113 Asn Tyr Leu His Ile Pro Val Asn Cys Pro Tyr Arg Ala Arg Val Ala
114      370                      375                      380
116 Asn Tyr Gln Arg Asp Gly Pro Met Cys Met Gln Asp Asn Gln Gly Gly
117 385                      390                      395                      400
119 Ala Pro Asn Tyr Tyr Pro Asn Ser Phe Gly Ala Pro Glu Gln Gln Pro
120                      405                      410                      415
122 Ser Ala Leu Glu His Ser Ile Gln Tyr Ser Gly Glu Val Arg Arg Phe
123                      420                      425                      430
125 Asn Thr Ala Asn Asp Asp Asn Val Thr Gln Val Arg Ala Phe Tyr Val
126                      435                      440                      445
128 Asn Val Leu Asn Glu Glu Gln Arg Lys Arg Leu Cys Glu Asn Ile Ala
129      450                      455                      460
131 Gly His Leu Lys Asp Ala Gln Ile Phe Ile Gln Lys Lys Ala Val Lys
132 465                      470                      475                      480
134 Asn Phe Thr Glu Val His Pro Asp Tyr Gly Ser His Ile Gln Ala Leu
135                      485                      490                      495
137 Leu Asp Lys Tyr Asn Ala Glu Lys Pro Lys Asn Ala Ile His Thr Phe
138                      500                      505                      510
140 Val Gln Ser Gly Ser His Leu Ala Ala Arg Glu Lys Ala Asn Leu

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147 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 3
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151 gcgcagaaag ctgatgtcct gaccactgga gctggtaacc cagtaggaga caaacttaat 120
152 gttattacag tagggccccc tggggccctt ctgtgtcagg atgtggtttt cactgatgaa 180
153 atggctcatt ttgaccgaga gagaattcct gagagagttg tgcattgctaa aggagcaggg 240
154 gcctttggct actttgaggt cacacatgac attaccaaact actccaaggc aaaggatatt 300
155 gagcatattg gaaagaagac tcccacgcga gttcggttct ccactgttgc tggagaatcg 360
156 ggttcagctg acacagttcg ggaccctcgt gggtttgcag tgaaatttta cacagaagat 420
157 ggtaactggg atctcgttgg aaataacacc cccattttct tcatcaggga tcccatattg 480
158 tttccatctt ttatccacag ccaaaagaga aatcctcaga cacatctgaa ggatccggac 540
159 atggtctggg acttctggag cctacgtcct gagtctctgc atcaggtttc tttcttggtc 600
160 agtgatcggg ggattccaga tggatccatc gccacatgaa tggatatgga tcacatactt 660
161 tcaagctggg taatgcaaat ggggaggcag tttattgcaa attccattat aagactgacc 720
162 agggcatcaa aaacctttct gttgaagatg cggcgagact ttcccaggaa gatcctgact 780
163 atggcatccg ggatcttttt aacgccattg ccacaggaaa gtacccctcc tggacttttt 840
164 acatccaggt catgacattt aatcaggcag aaacttttcc atttaatcca ttcgatctca 900
165 ccaaggtttg gcctcacaag gactaccctc tcatcccagt tggtaaactg gtcttaaac 960
166 ggaatccagt taattacttt gctgaggttg aacagatagc cttcgacca agcaacatgc 1020
167 cacctggcat tgaggccagt cctgacaaaa tgcttcaggg ccgccttttt gcctatcctg 1080
168 aactcaccg ccacgcctg ggacccaatt atcttcatat acctgtgaac tgtccctacc 1140
169 gtgctcgagt ggccaactac cagcgtgatg gcccgatgtg catgcaggac aatcagggtg 1200
170 gtgctccaaa ttactacccc aacagctttg gtgctccgga acaacagcct tctgcctgg 1260
171 agcacagcat ccaatattct ggagaagtgc ggagattcaa cactgccaat gatgataacg 1320
172 ttactcaggt gcgggcattc tatgtgaacg tgctgaatga ggaacagagg aaacgtctgt 1380
173 gtgagaacat tgccggccac ctgaaggatg cacaaatttt catccagaag aaagcggcca 1440
174 agaacttcac tgagggtccac cctgactacg ggagccacat ccaggctctt ctggacaagt 1500
175 acaatgctga gaagcctaag aatgcgatc acacctttgt gcagtccgga tctcacttgg 1560
176 cggcaaggga gaaggcaaat ctgtga
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 16
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
186 peptide
188 <400> SEQUENCE: 4
189 Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
190 1 5 10 15
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 16
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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200     peptide
202 <400> SEQUENCE: 5
203 Arg Gln Ile Lys Ile Phe Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
204   1             5             10             15
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 16
209 <212> TYPE: PRT
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
214     peptide
216 <400> SEQUENCE: 6
217 Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Phe Lys Lys
218   1             5             10             15
221 <210> SEQ ID NO: 7
222 <211> LENGTH: 16
223 <212> TYPE: PRT
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
228     peptide
230 <400> SEQUENCE: 7
231 Arg Gln Ile Lys Ile Phe Phe Gln Asn Arg Arg Met Lys Phe Lys Lys
232   1             5             10             15
235 <210> SEQ ID NO: 8
236 <211> LENGTH: 21
237 <212> TYPE: PRT
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
242     peptide
244 <400> SEQUENCE: 8
245 Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
246   1             5             10             15
248 Lys Lys Arg Lys Val
249           20
252 <210> SEQ ID NO: 9
253 <211> LENGTH: 12
254 <212> TYPE: PRT
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
259     motif
261 <400> SEQUENCE: 9
262 Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp
263   1             5             10
266 <210> SEQ ID NO: 10
267 <211> LENGTH: 6
268 <212> TYPE: PRT

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269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
273     peptide
275 <400> SEQUENCE: 10
276 Lys Lys Lys Arg Lys Val
277     1             5
280 <210> SEQ ID NO: 11
281 <211> LENGTH: 9
282 <212> TYPE: PRT
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
287     peptide
289 <400> SEQUENCE: 11
290 Arg Leu Gln Val Val Leu Gly His Leu
291     1             5
294 <210> SEQ ID NO: 12
295 <211> LENGTH: 19
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
302 <400> SEQUENCE: 12
303 gtgaaccgctc agatccgct                                19
306 <210> SEQ ID NO: 13
307 <211> LENGTH: 50
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
314 <400> SEQUENCE: 13
315 cgtctcgagt tatagatcag ctttcagctc gtccatgccg agagtgatcc        50
318 <210> SEQ ID NO: 14
319 <211> LENGTH: 30
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
326 <400> SEQUENCE: 14
327 ccgctagcgc taccggtcgc caccatggcc                        30
330 <210> SEQ ID NO: 15
331 <211> LENGTH: 42
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
338 <400> SEQUENCE: 15
339 cgtctcgagt tataatttgg acaggaacag gtggtggcgg cc                42

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/533,124

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Input Set : A:\SEQ LISTING-2 (WSU-9 US).txt

Output Set: N:\CRF4\05102005\J533124.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number